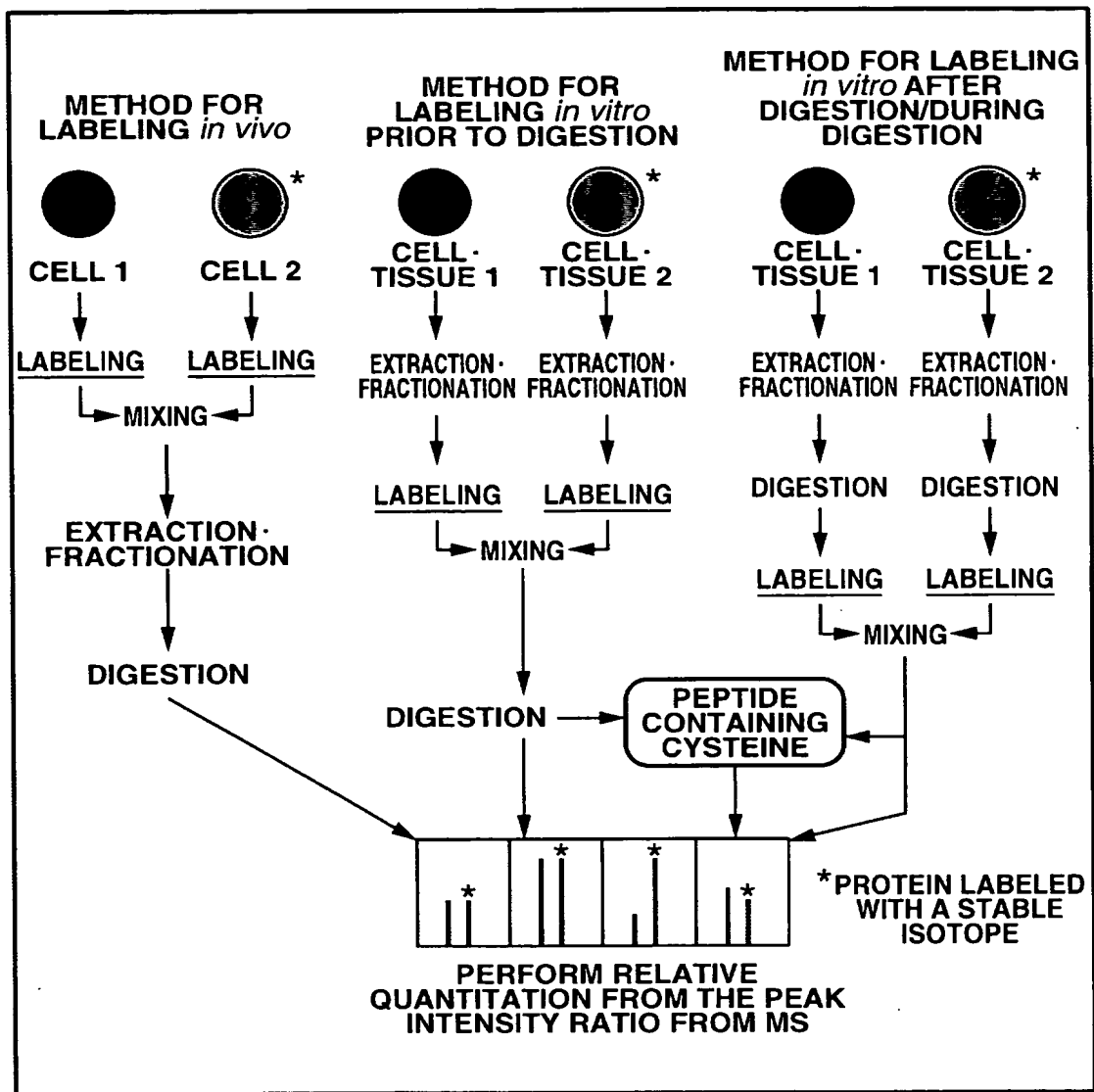
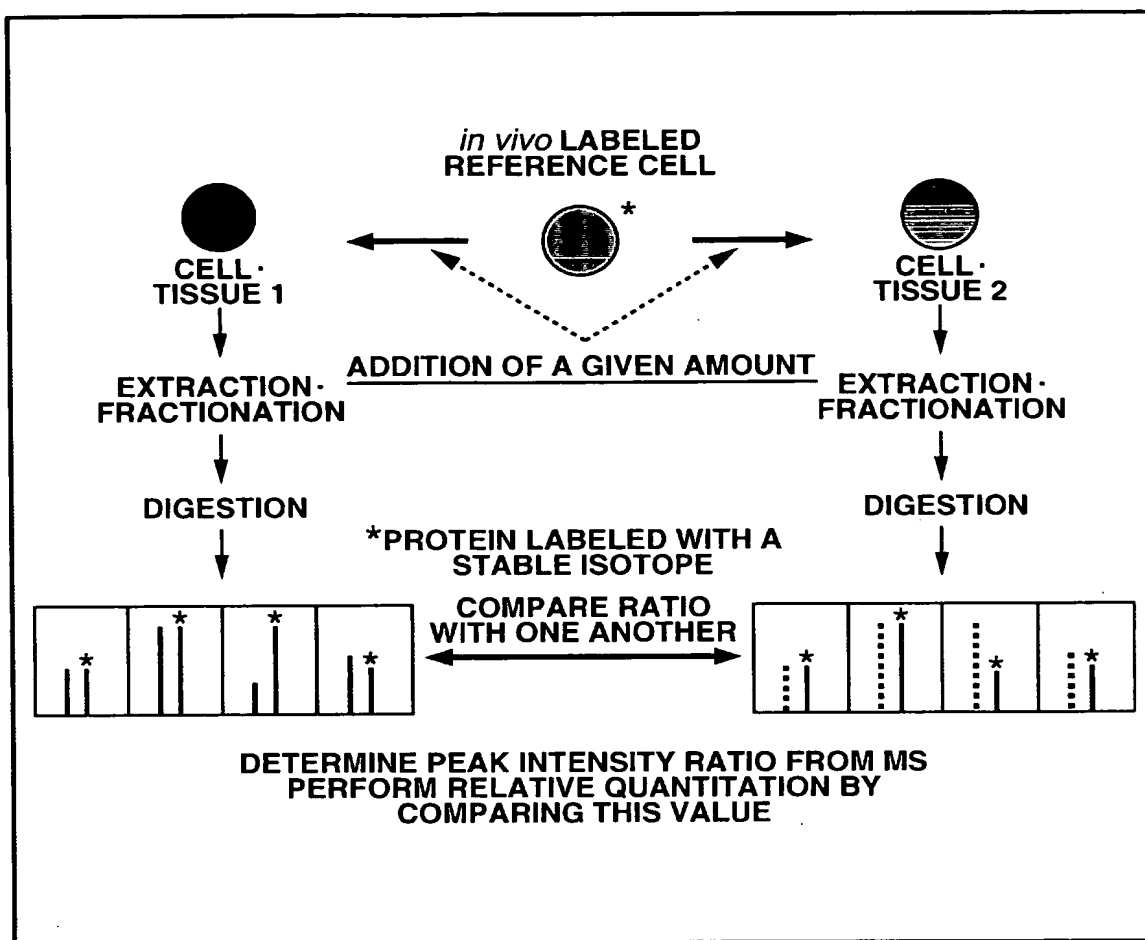


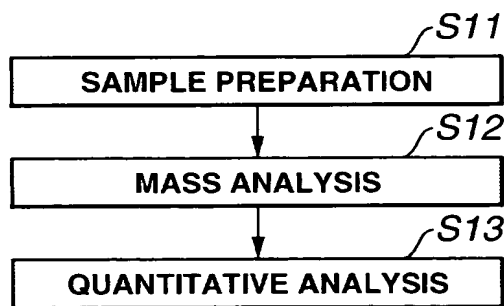
**FIG.1**



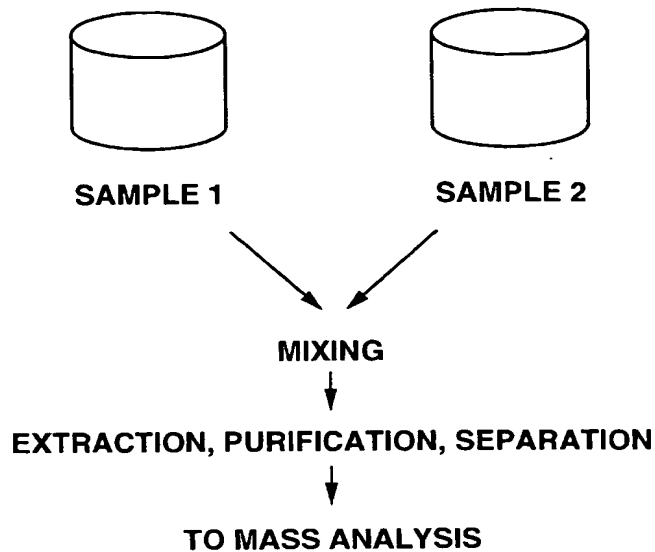
# FIG.2



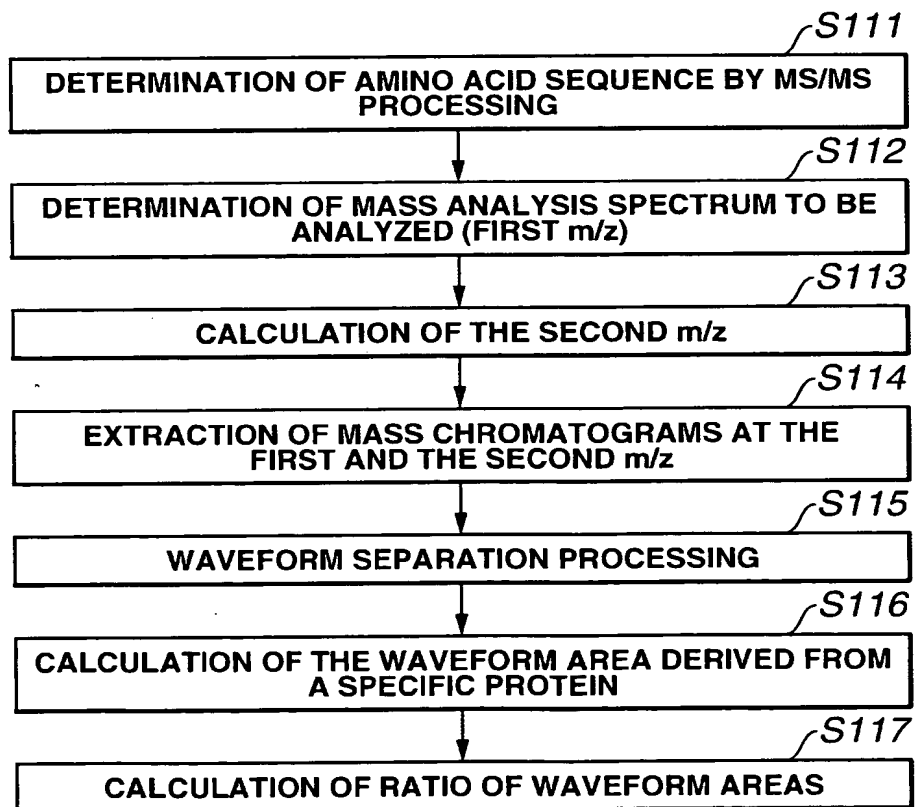
# FIG.3



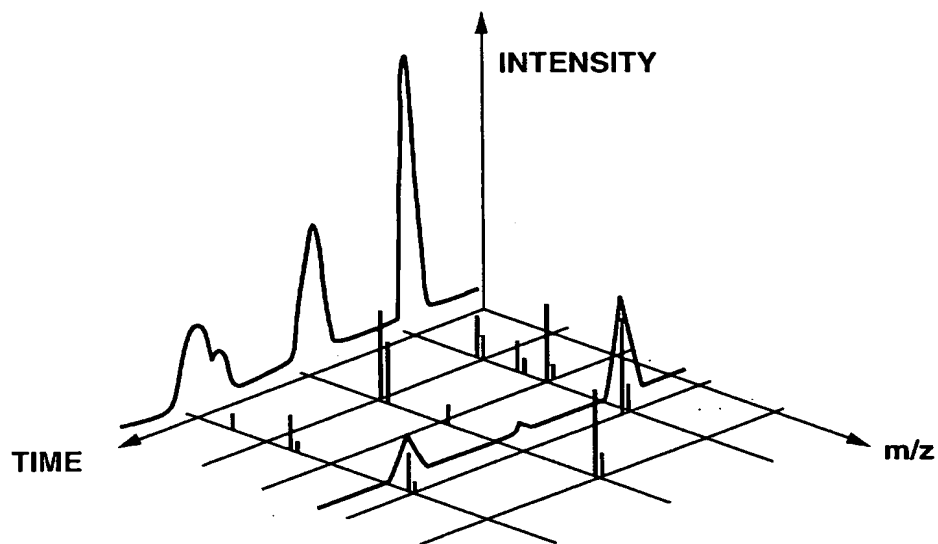
# FIG.4



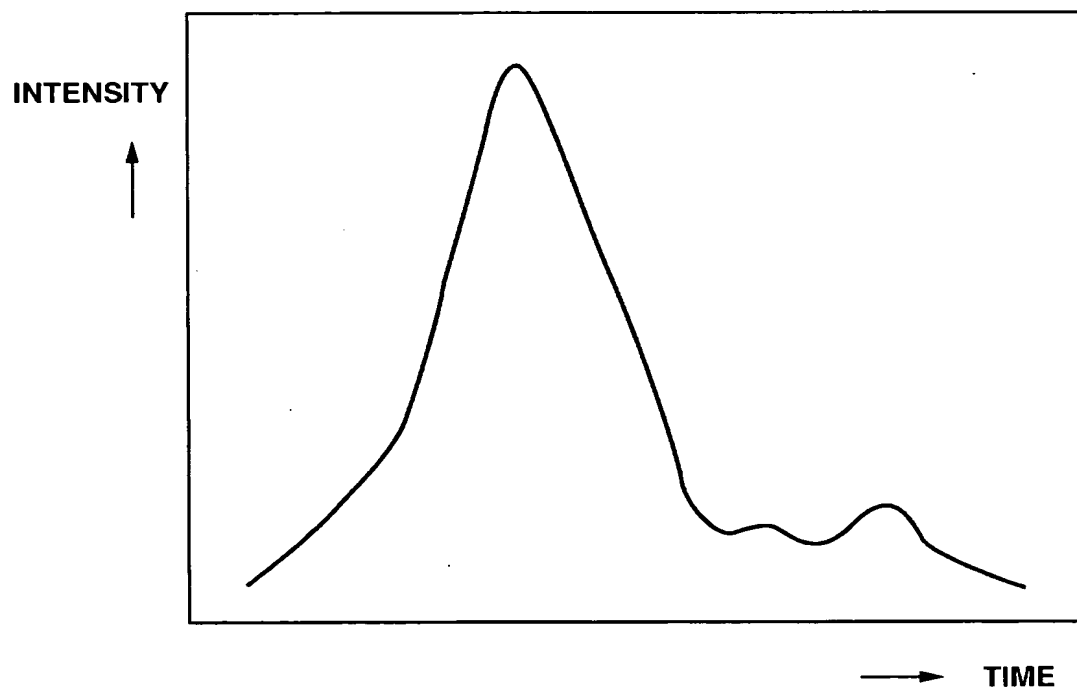
# FIG.5



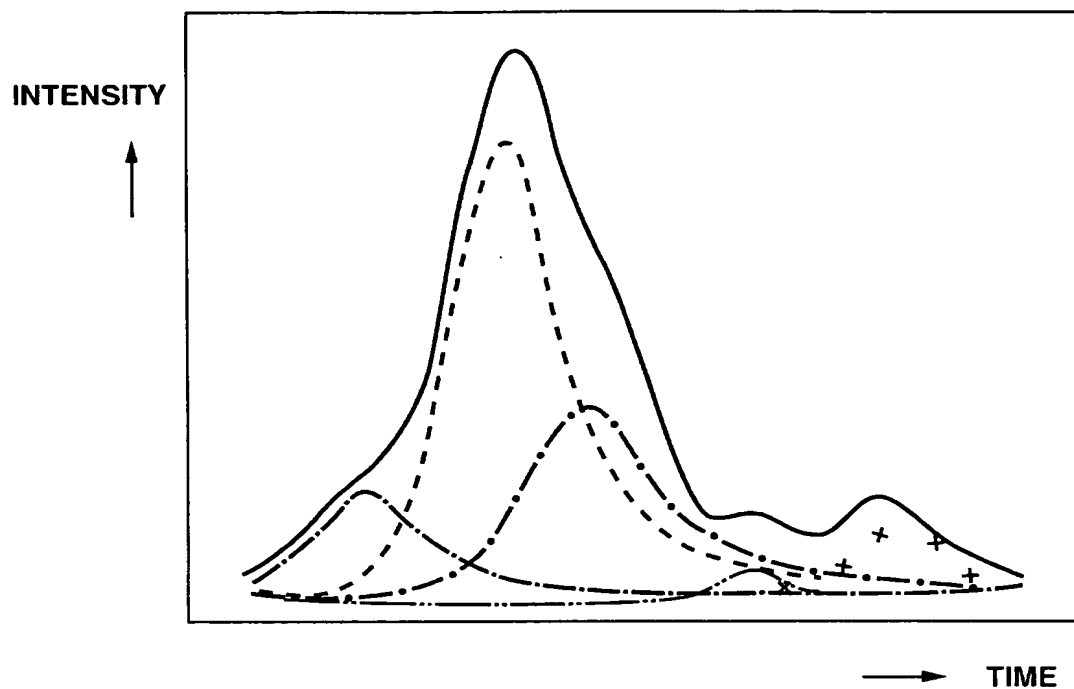
**FIG.6**



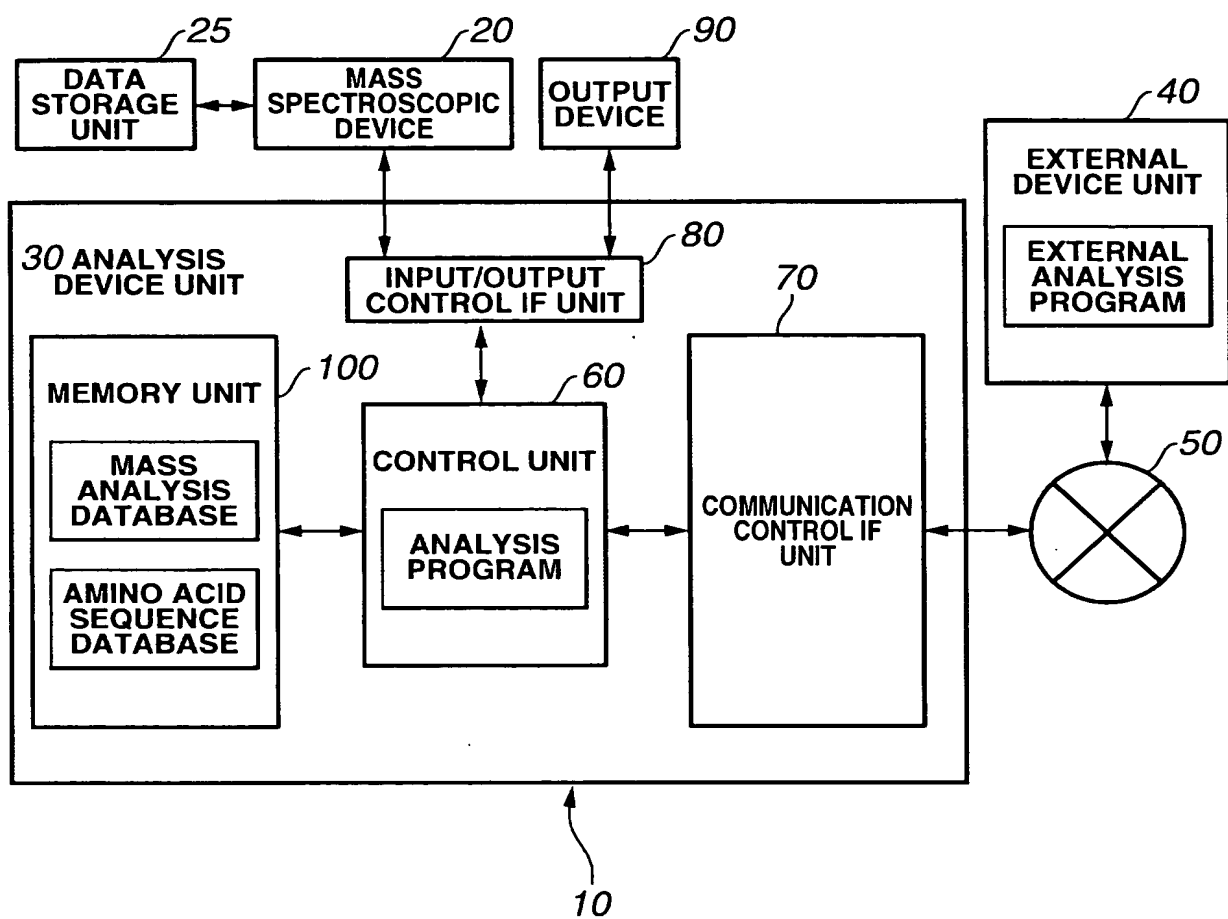
**FIG.7**



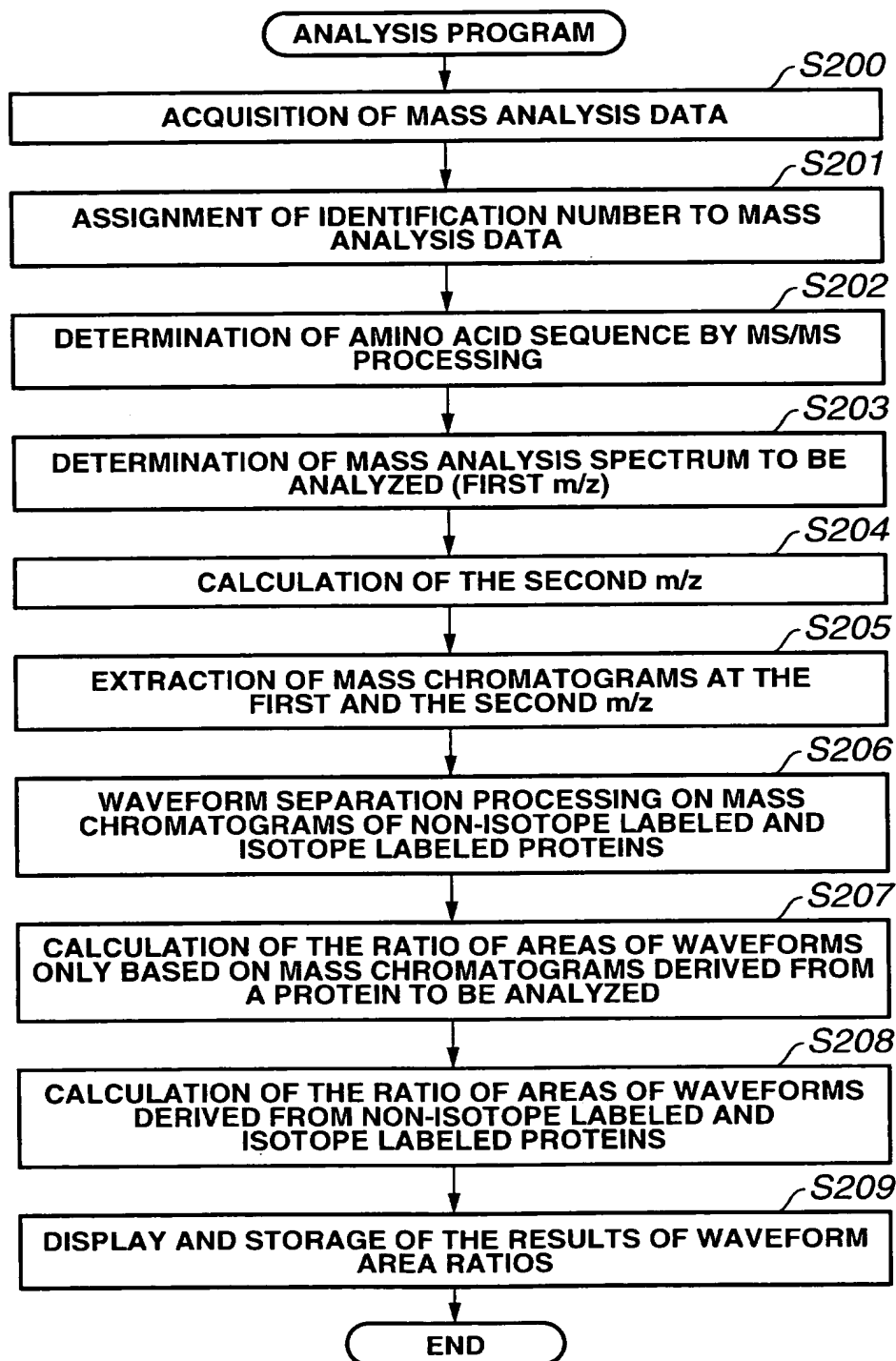
**FIG.8**



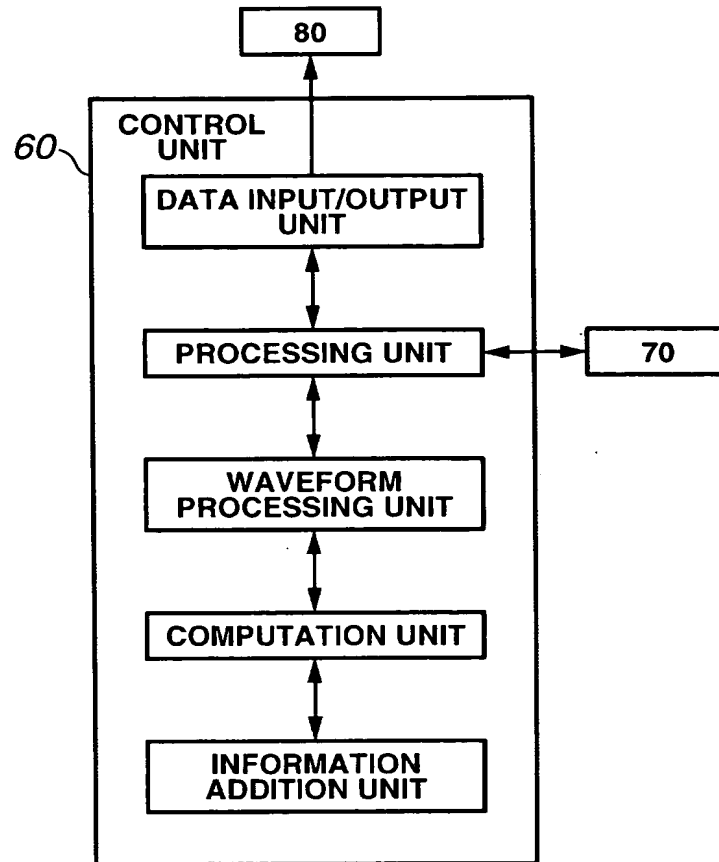
**FIG.9**



# FIG.10

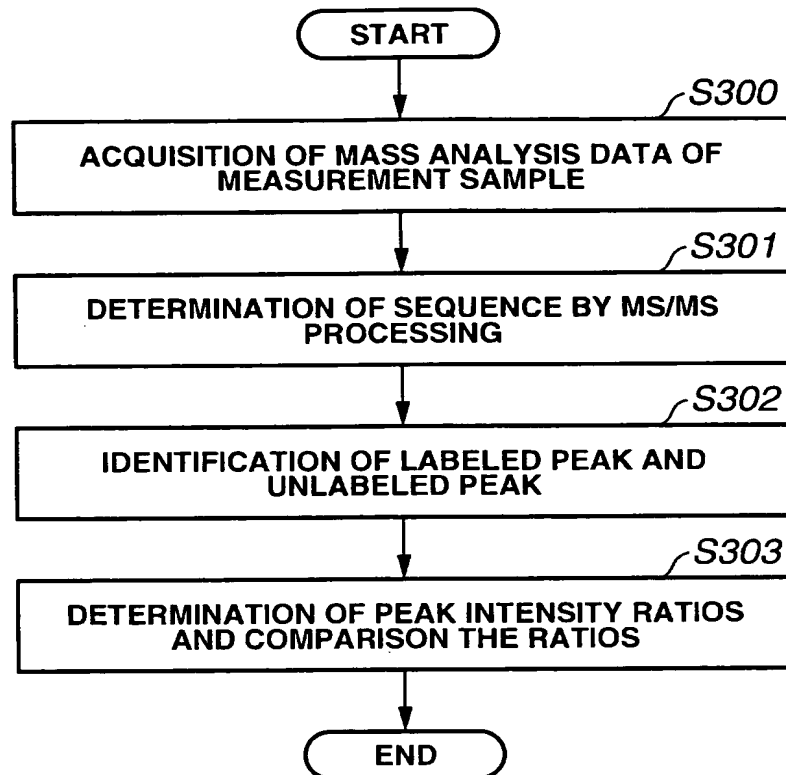


**FIG.11**

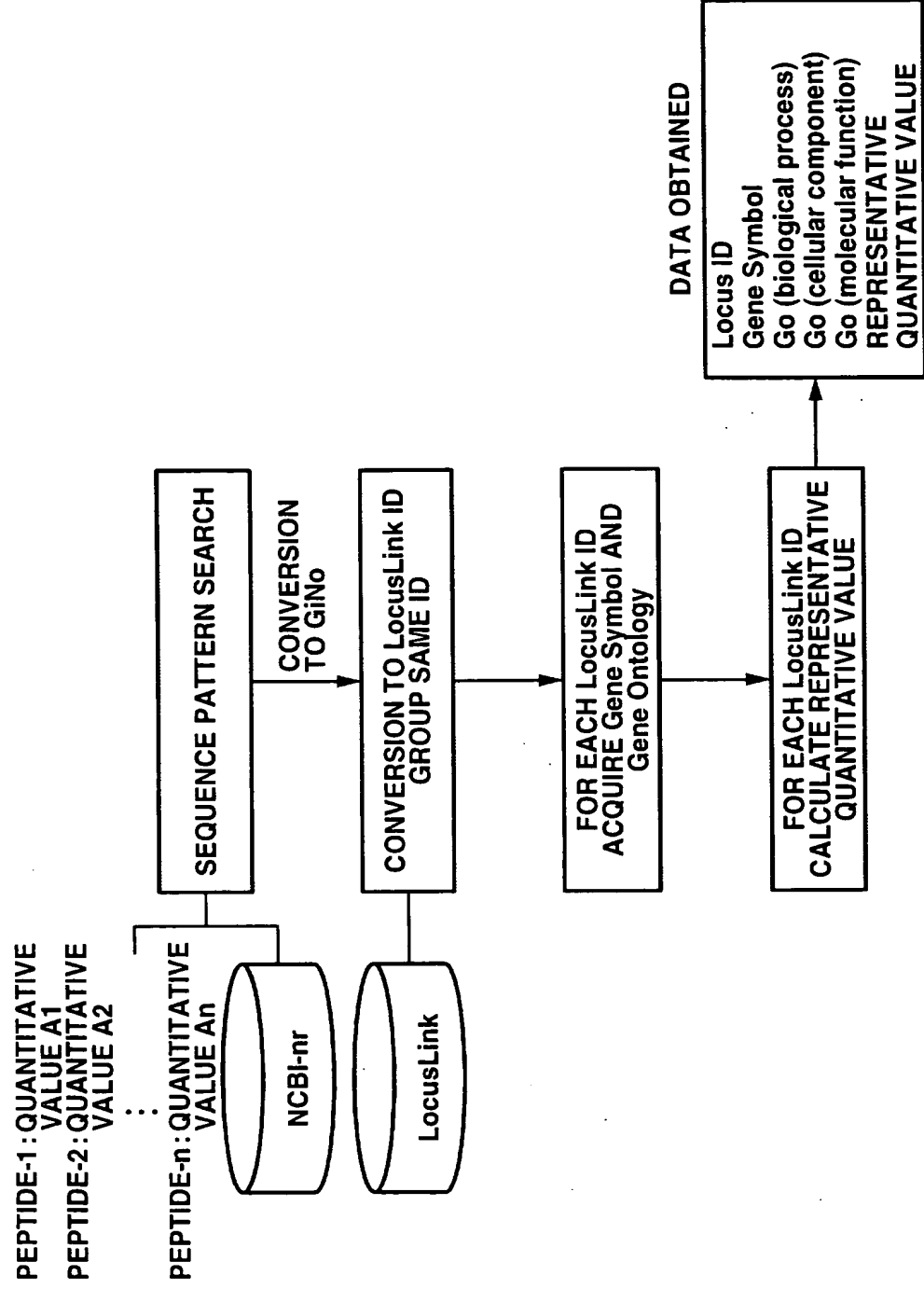




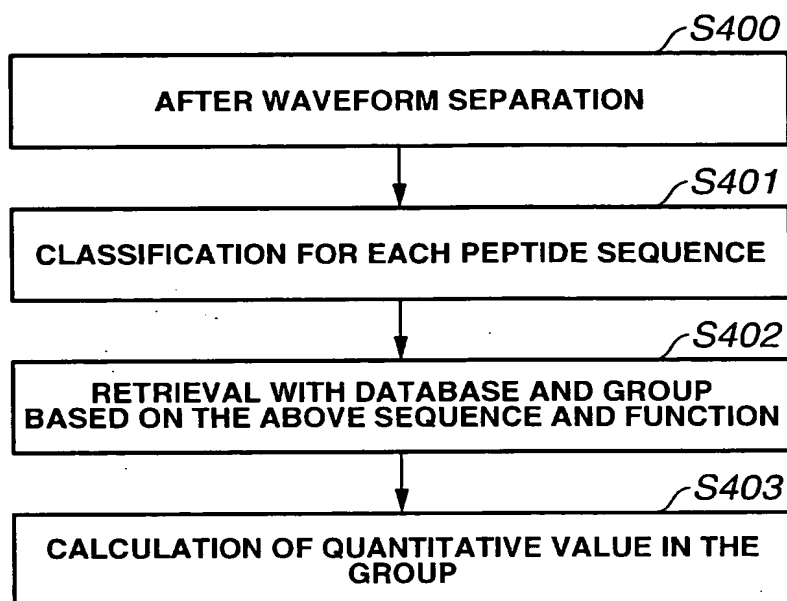
**FIG.12**



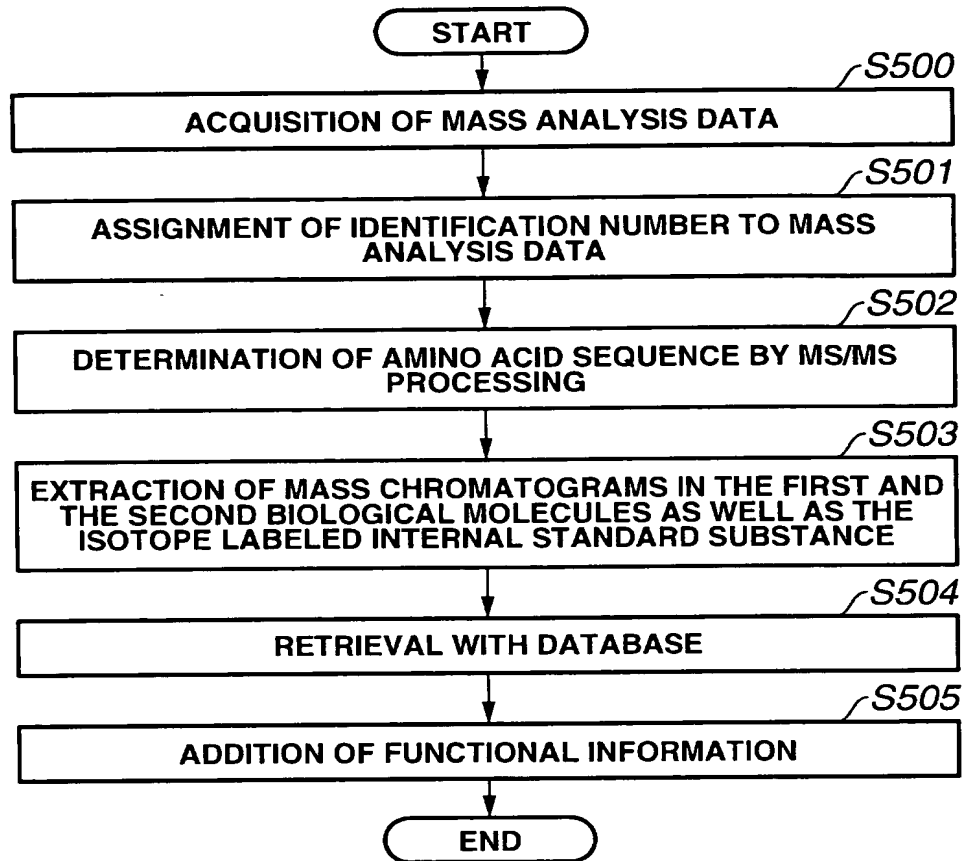
**FIG.13**



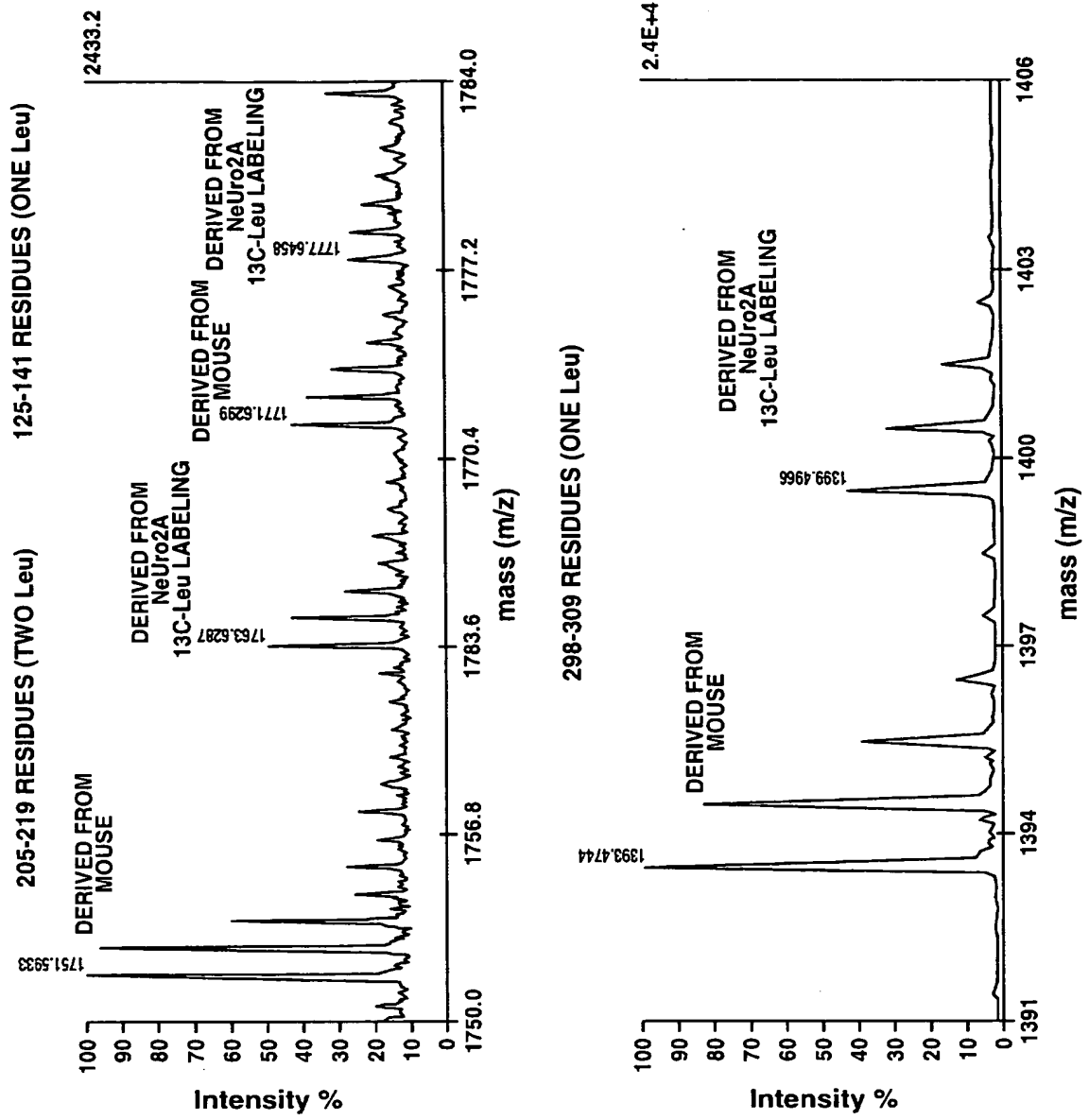
# FIG.14



# FIG.15

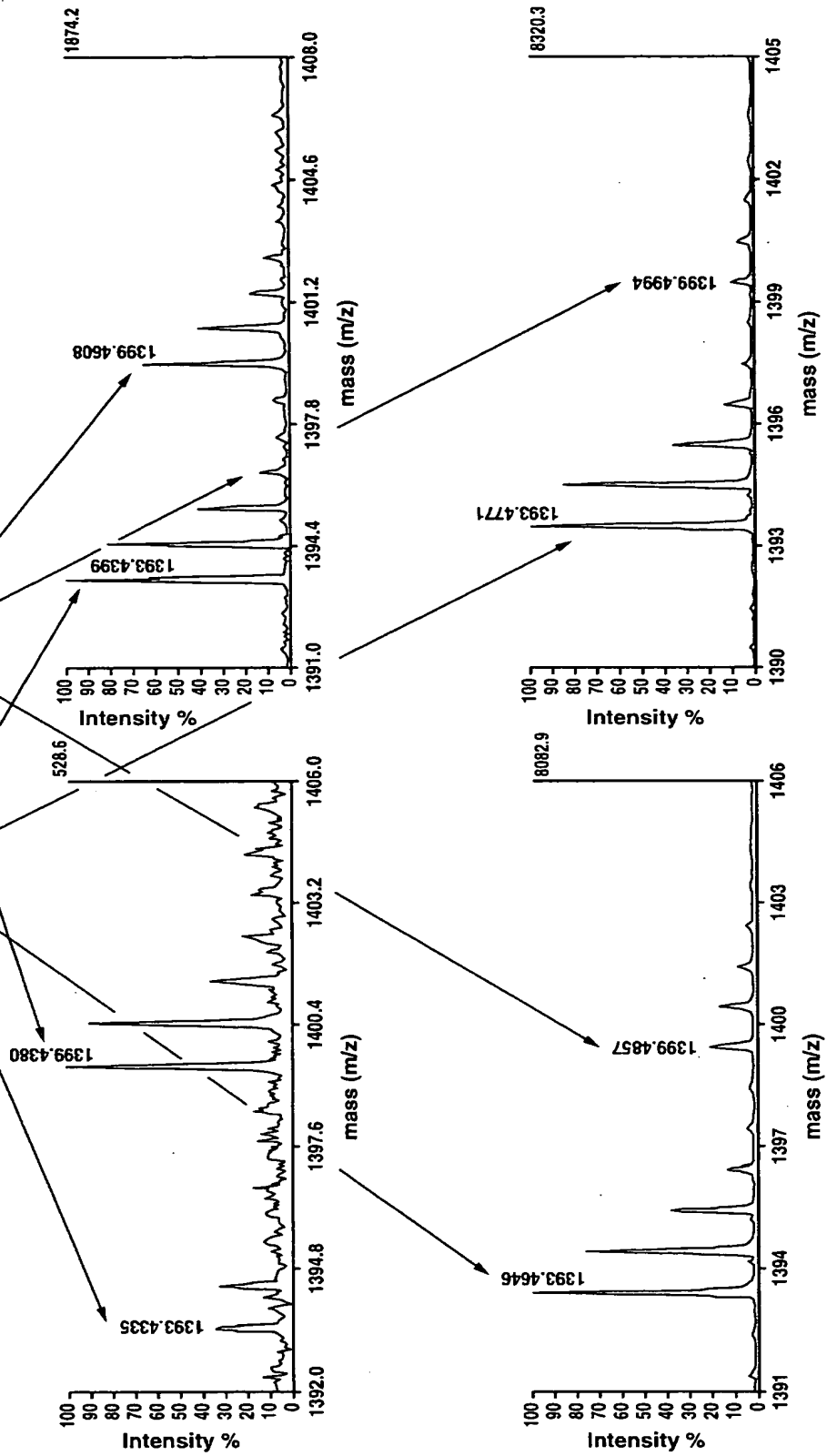


# FIG.16

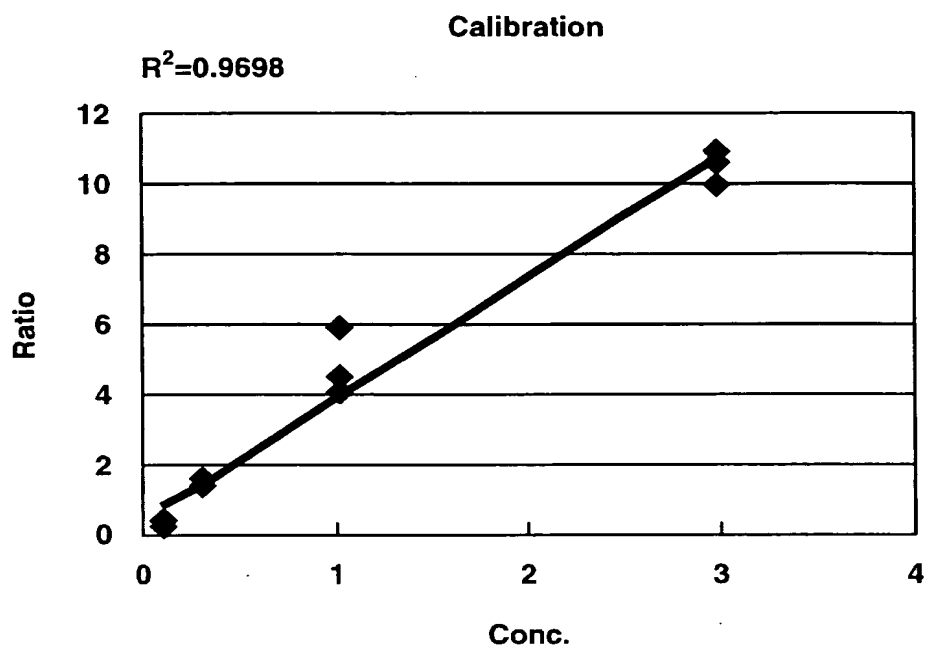


# FIG.17

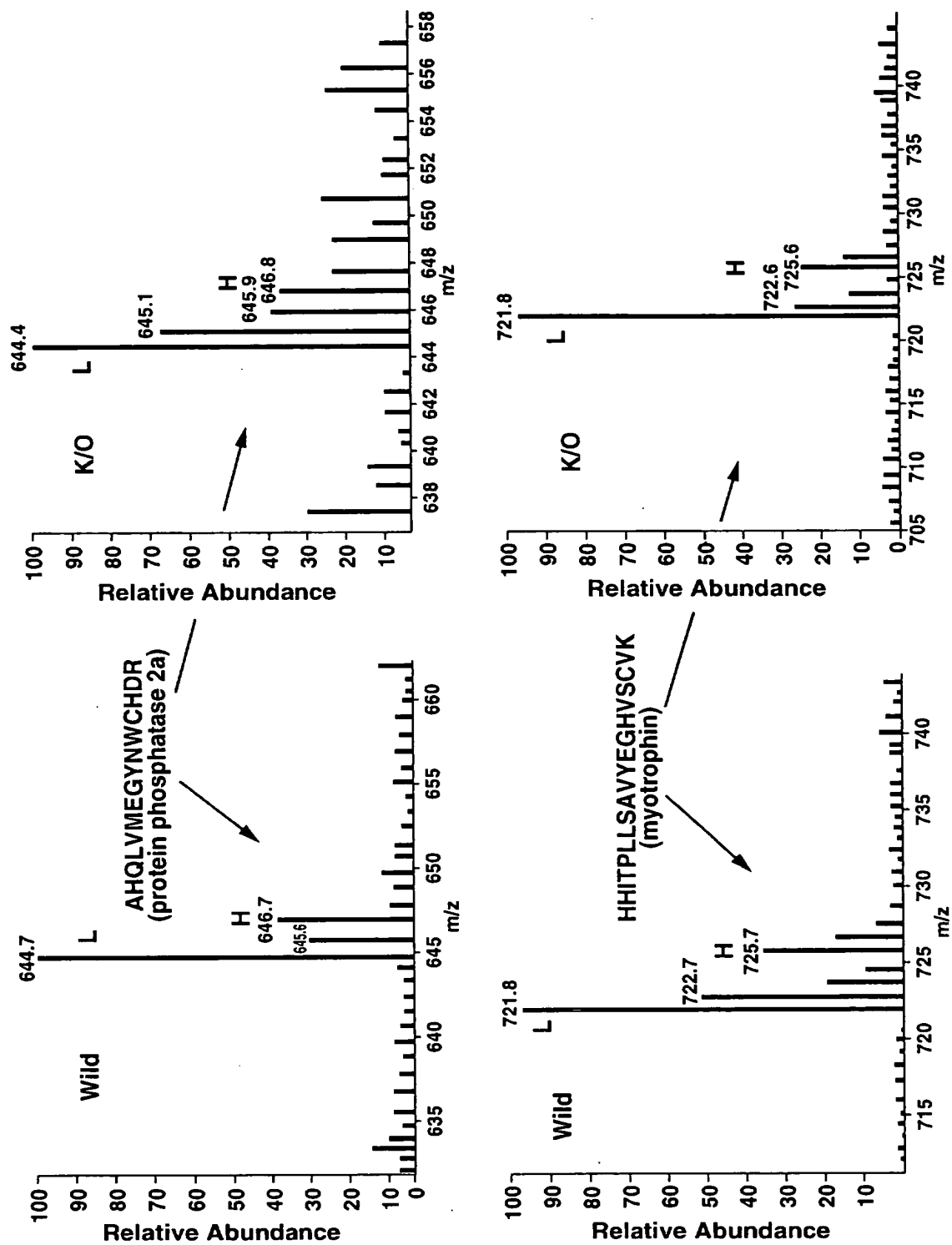
REGARDING Dose Response, 298-309 RESIDUES IN CMDH  
(LEFT SIDE IS DERIVED FROM MOUSE BRAIN, RIGHT SIDE IS  
DERIVED FROM Neuro2A AND <sup>13</sup>C LABELINGx6 ON Leu)



# FIG.18

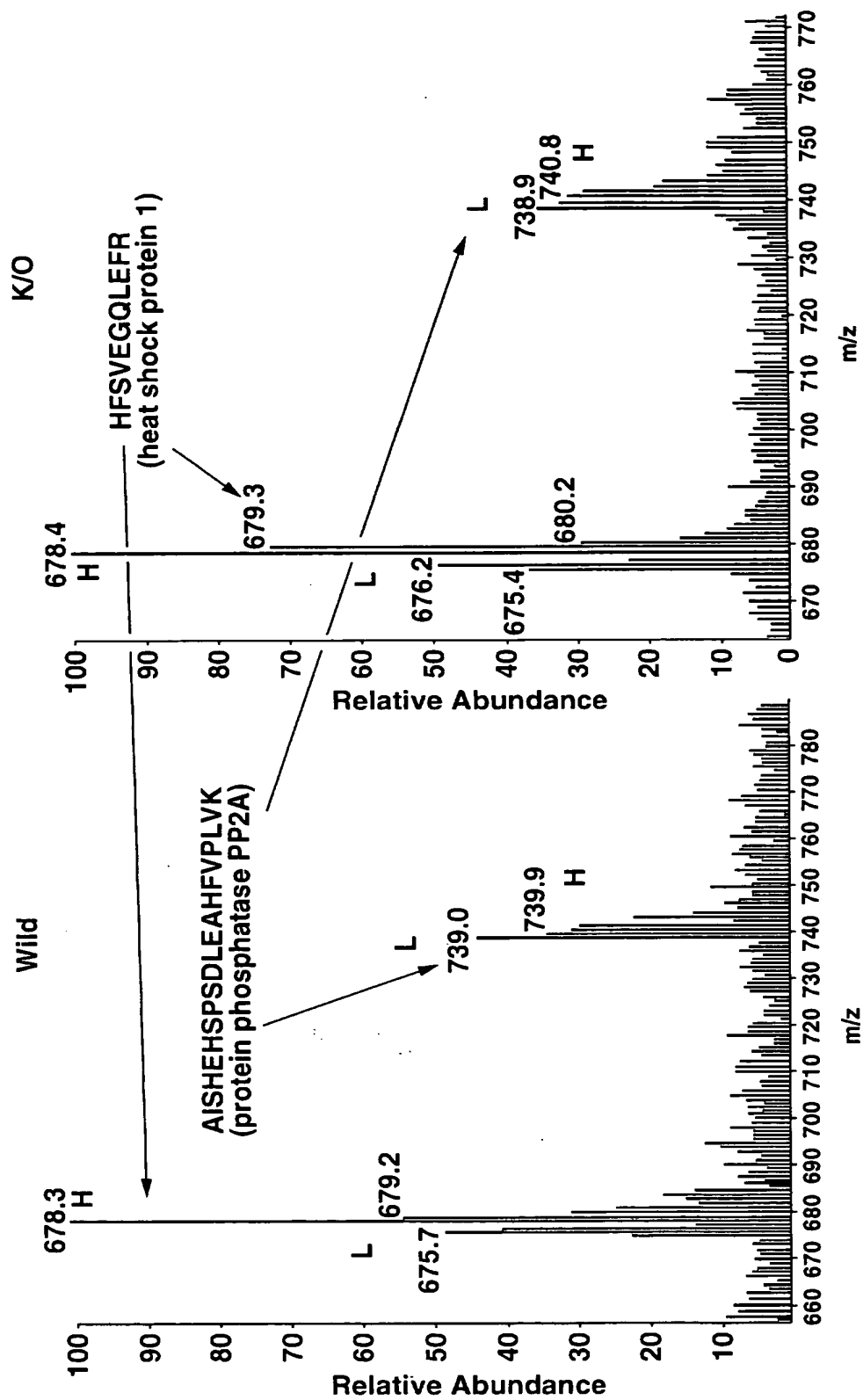


**FIG.19**





**FIG.20**



# FIG.21

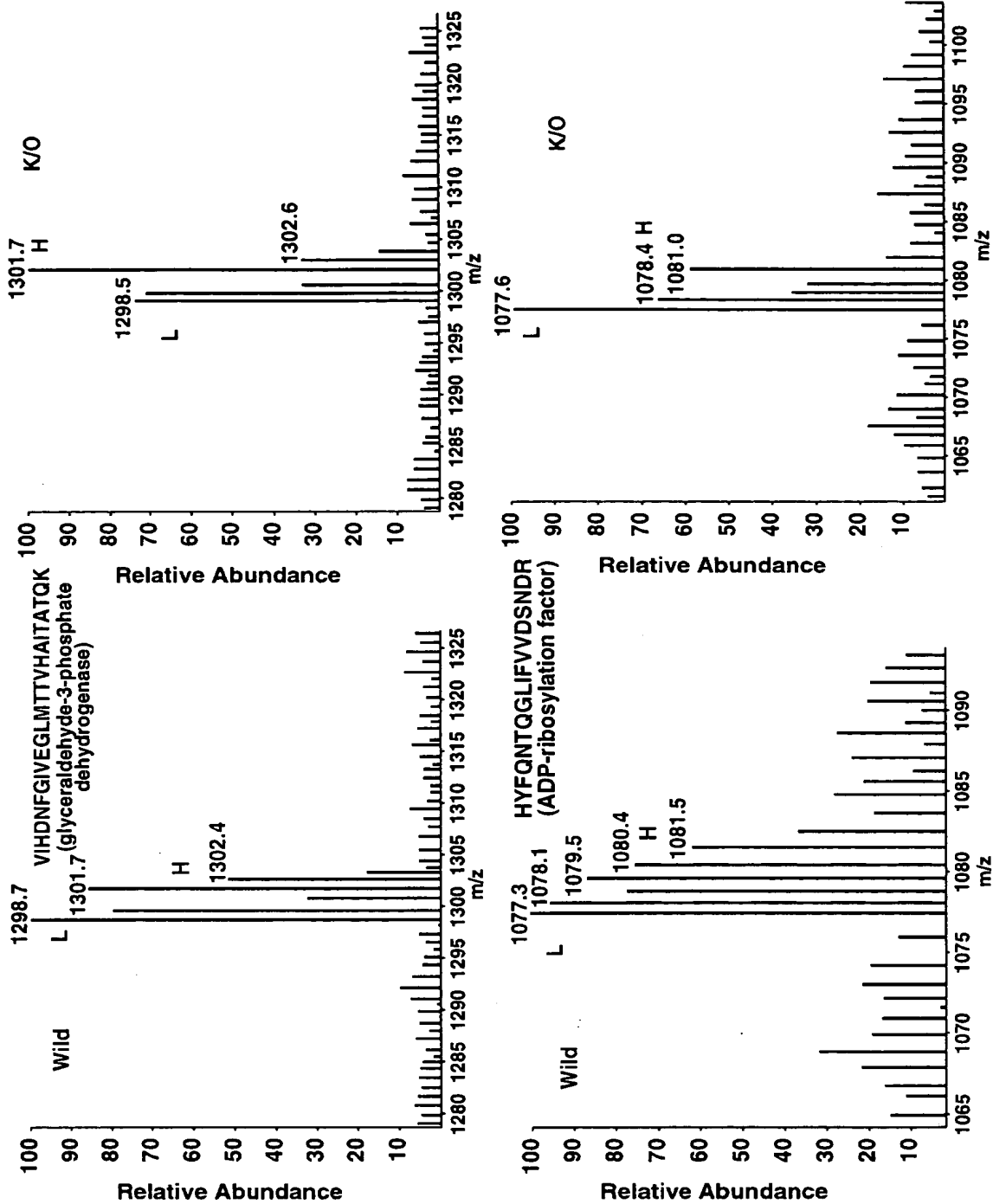
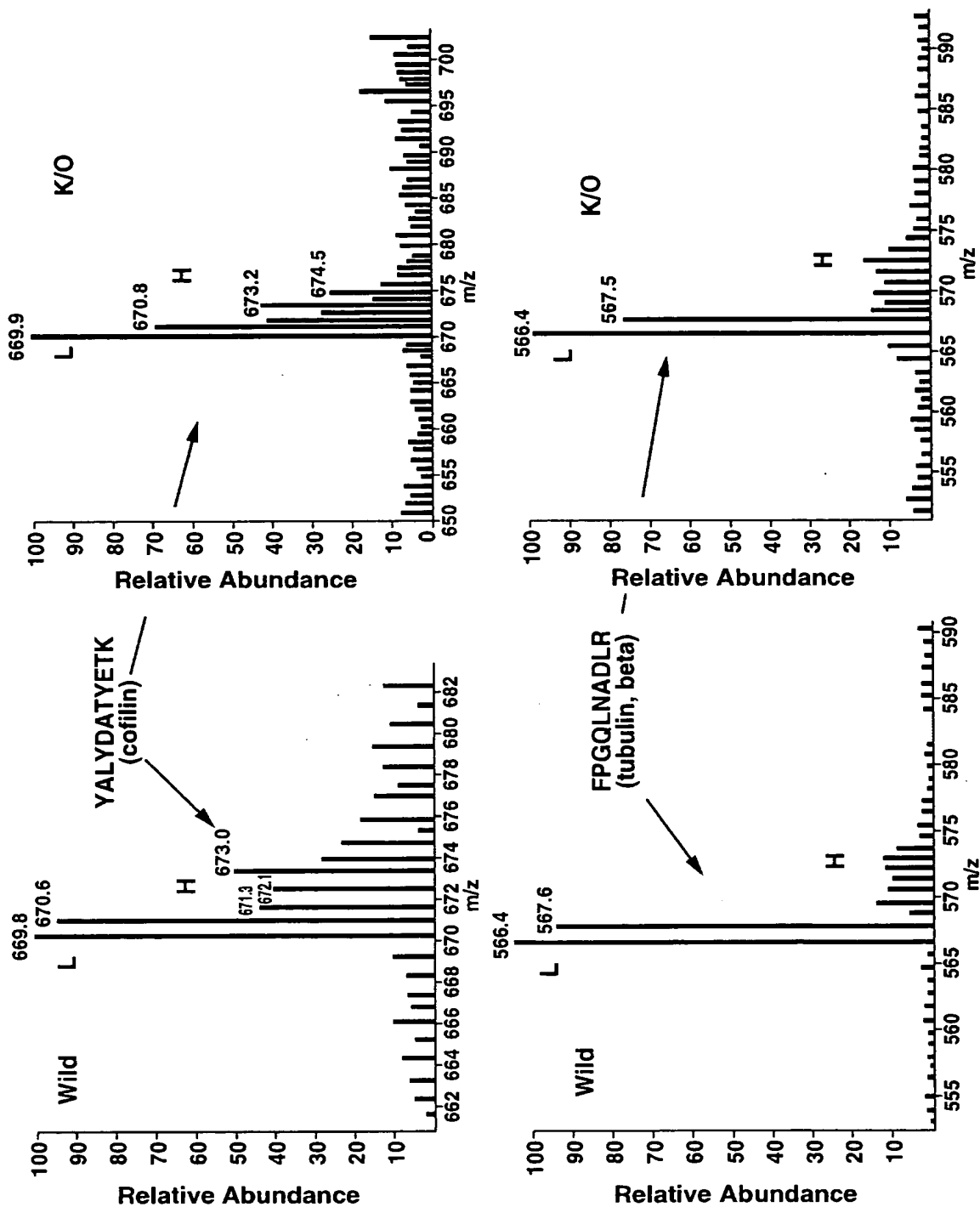
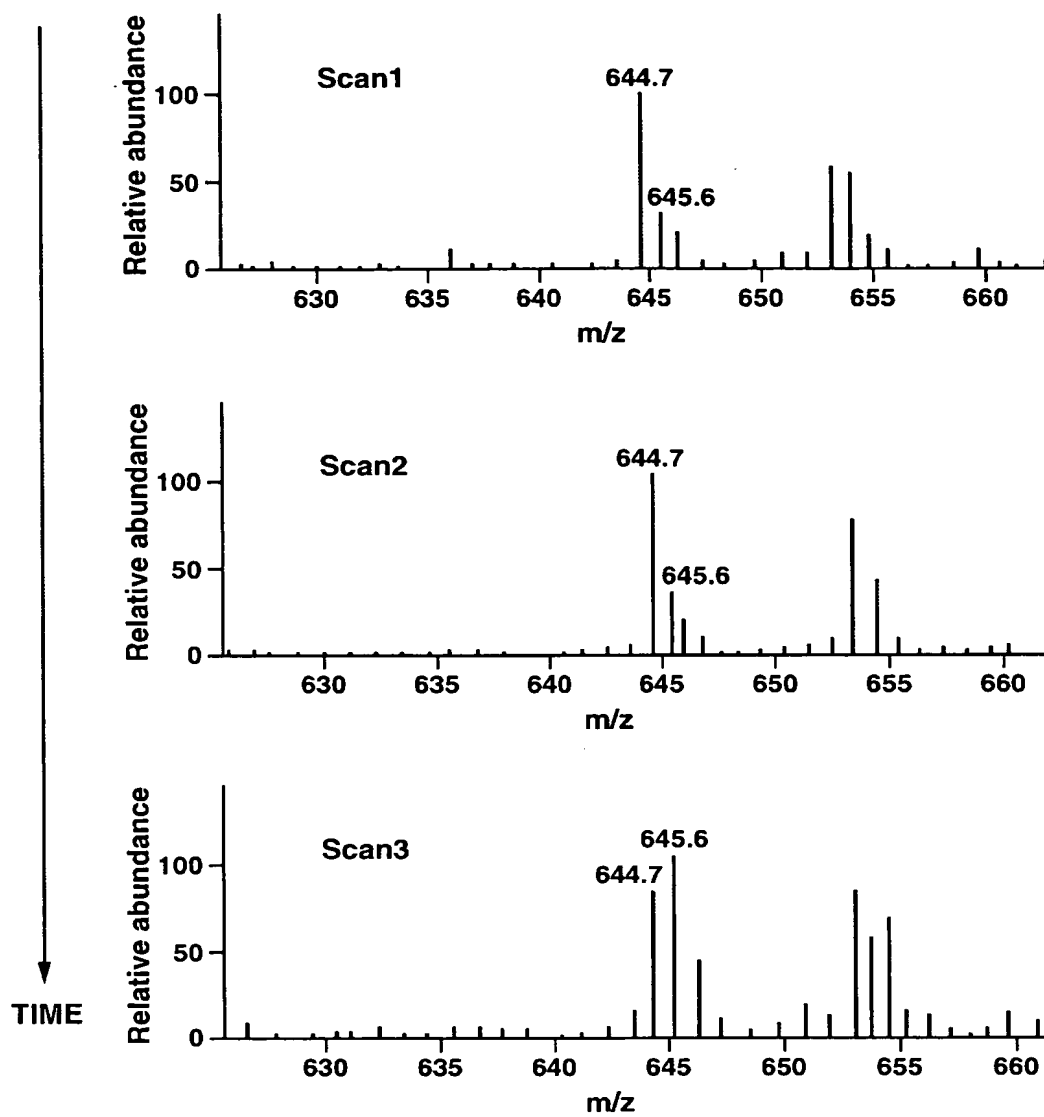


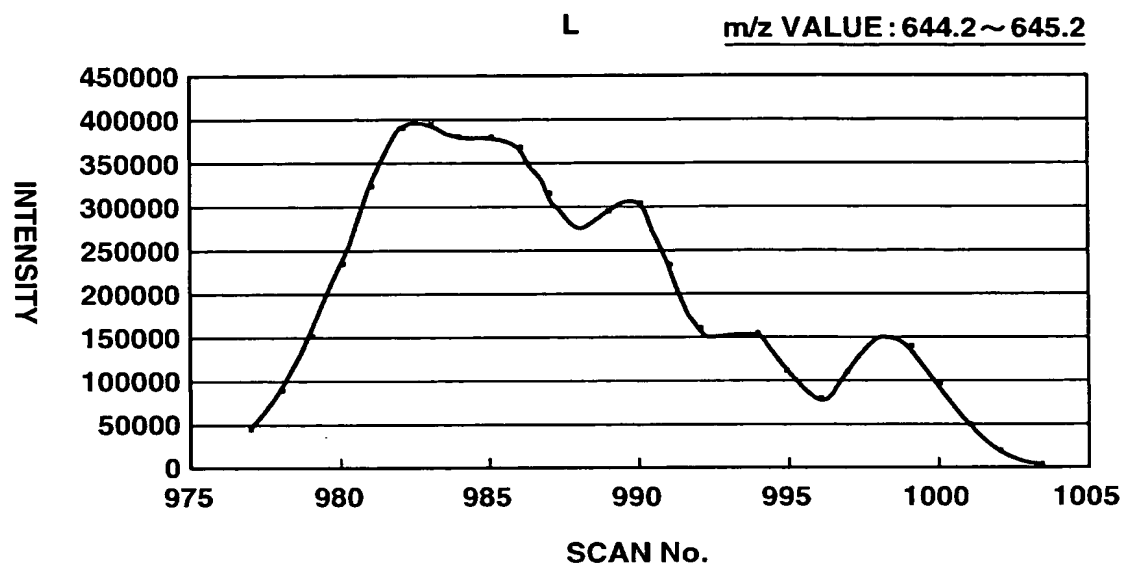
FIG.22



# FIG.23



# FIG.24



# FIG.25

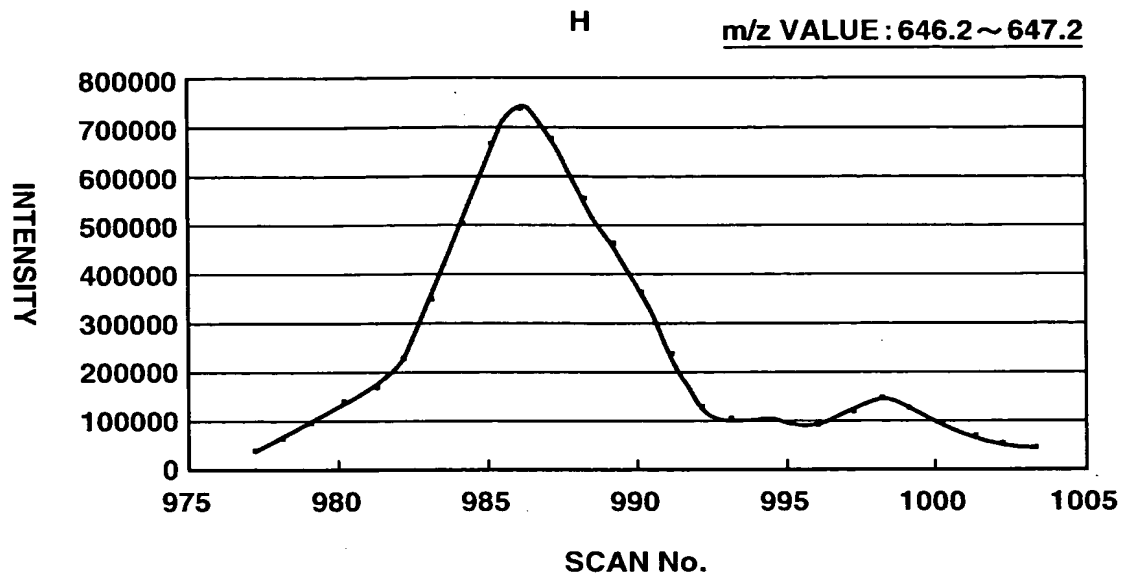


FIG.26A

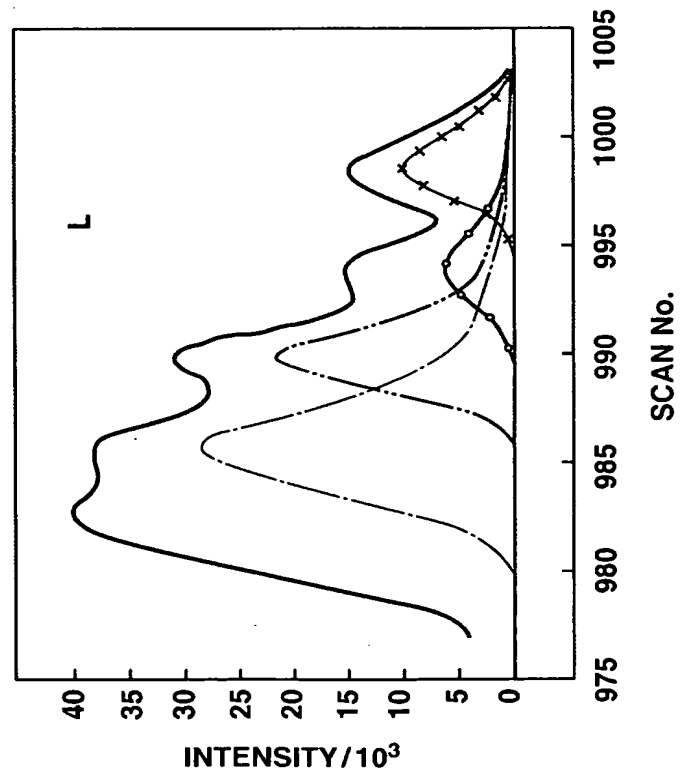
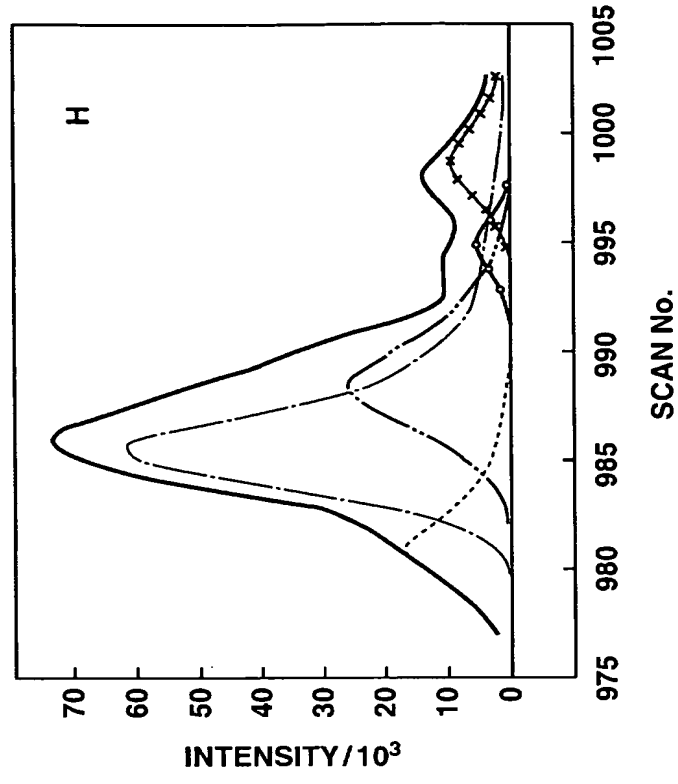


FIG.26B



# FIG.27

PEPTIDE SEQUENCE (PROTEIN NAME)	Wild PEAK INTENSITY RATIO/KNOCK OUT PEAK INTENSITY RATIO *LABELED MOLECULE WITH THE SAME SEQUENCE WAS USED AS THE INTERNAL STANDARD	Wild PEAK INTENSITY RATIO/KNOCK OUT PEAK INTENSITY RATIO **LABELED MOLECULE WITH A DIFFERENT SEQUENCE WAS USED AS THE INTERNAL STANDARD
SEQUENCE NO.1 : AHQLVMEGYNWCHDR (protein phosphatase 2a) SEE FIG. 10	2.92/3.09=0.95	2.81/3.82=0.74 LABELED MOLECULE WITH THE SEQUENCE NO. 2 WAS USED AS THE INTERNAL STANDARD
SEQUENCE NO.2 : HHITPLLSAVYEGHVSCVK (myotrophin) SEE FIG. 10	2.85/3.97=0.72	2.96/3.21=0.92 LABELED MOLECULE WITH THE SEQUENCE NO. 1 WAS USED AS THE INTERNAL STANDARD
SEQUENCE NO.3 : HFSVEGQLEFR (heat shock protein 1) SEE FIG. 11	0.45/0.46=0.97	2.58/3.03=0.85 LABELED MOLECULE WITH THE SEQUENCE NO. 4 WAS USED AS THE INTERNAL STANDARD
SEQUENCE NO.4 : AISHEHSPSDLEAHFVPLVK (protein phosphatase PP2A) SEE FIG. 11	2.35/2.14=1.10	0.41/0.33=1.23 LABELED MOLECULE WITH THE SEQUENCE NO. 3 WAS USED AS THE INTERNAL STANDARD
SEQUENCE NO.5 : VIHDNFGIVEGLMTTVHAIT ATQK (glyceraldehyde-3-phosphate de hydrogenase) SEE FIG. 12	1.18/0.73=1.61	1.86/2.07=0.90 LABELED MOLECULE WITH THE SEQUENCE NO. 6 WAS USED AS THE INTERNAL STANDARD
SEQUENCE NO.6 : HYFQNTQNTQGLIFVVDSDNR (ADP-ribosylation factor) SEE FIG. 12	1.84/1.86=0.99	0.89/1.18=0.75 LABELED MOLECULE WITH THE SEQUENCE NO. 5 WAS USED AS THE INTERNAL STANDARD
SEQUENCE NO.7 : YALYDATYETK (cofilin) SEE FIG. 13	2.17/2.60=0.83	10.8/9.2=1.17 LABELED MOLECULE WITH THE SEQUENCE NO. 8 WAS USED AS THE INTERNAL STANDARD
SEQUENCE NO.8 : FPGQLNADLR (tubulin, beta) SEE FIG. 13	11.38/9.4=1.21	2.28/2.66=0.86 LABELED MOLECULE WITH THE SEQUENCE NO. 7 WAS USED AS THE INTERNAL STANDARD



# FIG.28

SEQUENCE	QUANTITATION NUMBER
ALVLELCCNDESGEDVEVPYVR	1.51091043
KPLLESGTLGTK	1.351344211
NFPNAIEHTLQWAR	0.379425372
NFPNAIEHTLQWAR	1.006616361
NFPNAIEHTLQWAR	0.498511448
NFPNAIEHTLQWAR	0.620944209
NFPNAIEHTLQWAR	0.744001926
NFPNAIEHTLQWAR	0.39584672
NFPNAIEHTLQWAR	0.569211695
NFPNAIEHTLQWAR	0.682017147
NFPNAIEHTLQWAR	0.362867677
NFPNAIEHTLQWAR	1.20440506
NFPNAIEHTLQWAR	1.443092102
NFPNAIEHTLQWAR	0.767798114
NFPNAIEHTLQWAR	1.736296952
NFPNAIEHTLQWAR	0.2713649
NFPNAIEHTLQWAR	2.245947181
NFPNAIEHTLQWAR	3.110330946
NFPNAIEHTLQWAR	0.251063062
YFLVGAGAIGCELLK	21.56982391
YFLVGAGAIGCELLK	0.651272581
YFLVGAGAIGCELLK	8.513072128
YFLVGAGAIGCELLK	5.037104157

## FIG.29

**SEARCH TARGET : ALVLELCCNDESGEDVEVPYVR**

**IDENTIFIED PROTEINS:**

gi | 23510340 | ref | NP\_695012.1 |  
gi | 35830 | emb | CAA40296.1 |  
gi | 24485 | emb | CAA37078.1 |

**SEARCH TARGET : KPLLESGTLGTK**

**IDENTIFIED PROTEINS:**

gi | 23510340 | ref | NP\_695012.1 |  
gi | 35830 | emb | CAA40296.1 |  
gi | 24485 | emb | CAA37078.1 |

**SEARCH TARGET : NFPNAIEHTLQWAR**

**IDENTIFIED PROTEINS:**

gi | 23510340 | ref | NP\_695012.1 |  
gi | 35830 | emb | CAA40296.1 |  
gi | 24485 | emb | CAA37078.1 |

**SEARCH TARGET : YFLVGAGAIGCELLK**

**IDENTIFIED PROTEINS:**

gi | 23510340 | ref | NP\_695012.1 |  
gi | 35830 | emb | CAA40296.1 |  
gi | 24485 | emb | CAA37078.1 |

## FIG.30A

gi | 23510340 | ref | NP\_695012.1 |  
gi | 35830 | emb | CAA40296.1 |  
gi | 24485 | emb | CAA37078.1 |

## FIG.30B

**official\_symbol : UBE1**

**product : ubiquitin-activating enzyme E1**

**go(molecular function) :**

**ATP binding.  
ligase activity.  
ubiquitin activating enzyme activity.**

**go(biological process) :**

**DNA replication.  
ubiquitin cycle.**